CLAIM AMENDMENTS

Claims 1 to 27 (canceled)

Claim 28 (Currently Amended)

An isolated nucleic acid epecific to mycobacteria of M.tuberculosis complex having a nucleotide sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the a complement of SEQ ID No: 1, and the a complement of SEQ ID No: 2.

Claim 29 (Currently Amended)

An isolated nucleic acid specific to mycobacteria of
M.tuberculosis complex having a nucleotide sequence
selected from the group consisting of SEQ ID No: 1 and the
a complement of SEQ ID No: 1.

Claim 30 (Currently Amended)

An isolated nucleic acid specific to mycobacteria of M.tuberculosis complex which mycobacteria is different from BCC, whereas said nucleic acid has having a nucleotide sequence selected from the group consisting of SEQ ID No: 2 and—the—a complement of SEQ ID No: 2.

Claim 31 (Previously Presented)

A cloning or expression vector containing a nucleic acid sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 32 (previously presented)

A vector of claim 31 which is a plasmid selected from the group consisting of pRegX3Bc1 and pRegX3Mt1 deposited at CNCM under Nos. I-1765 and I-1766, respectively.

Claim 33 (Canceled)

Claim 34 (Previously Presented)

A nucleotide probe or nucleotide primer comprising 24 consecutive nucleotides selected from a sequence selected from the group consisting of SEQ ID No:1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 35 (Currently Amended)

A nucleotide probe or nucleotide primer that

hybridizes at 68°C in a 5x6SC hybridization buffer with one
of the sequences comprising a sequence selected from the

group consisting of sequence SEQ ID No: 1, or the a complement of SEQ ID No: 1, or their a corresponding RNA sequence[e] of sequence SEQ ID No: 1 or a complement of SEQ ID No: 1, or their and a corresponding gene of said corresponding RNA sequences, and that contains a maximum of 21 base pairs.

Claim 36 (Currently Amended)

A nucleotide probe or nucleotide primer that
hybridizes at 68°C in a 5xSSC hybridization buffer with one
of the sequences having a sequence comprising two
successive sequences SEQ ID No: 1 followed by a sequence
SEQ ID No: 2 or their corresponding RNA sequences or their
corresponding gene, and that contains a maximum of 21 base
pairs.

Claim 37 (Currently Amended)

A nucleotide probe for detection of specific sequences of nucleic acids of M.tuberculosis complex other than BCG wherein said probe consists of 21 base pairs having a sequence of a region of sequence SEQ ID No: 2 comprising the a GAG codon in positions 40 to 42 or the a complement of said region.

Claim 38 (Currently Amended)

A nucleotide probe for detection of specific sequences of nucleic acids of M. Eubersulosis complex other than BCC comprising a sequence composed of nucleotides in positions 31 to 51 of SEQ ID No: 2 or—the—a_complement of said sequence.

Claim 39 (Canceled)

Claim 40 (Currently Amended)

A nucleotide probe of claim 37 comprising the sequence SEQ ID No: 2 or the a complement of SEQ ID No: 2.

Claim 41 (Currently Amended)

A nucleotide probe or nucleotide primer that

hybridizes at 68°C in a 5xSSC hybridization buffer with

labeled by digoxygenin comprising one of the sequences

selected from the group consisting of SEQ ID No: 1, SEQ ID

No: 2, the a complement of SEQ ID No: 1, and the a

complement of SEQ ID No: 2, their a corresponding RNA

sequences or their sequence selected from the group

consisting of SEQ ID No: 1, SEQ ID NO:2 and a corresponding

gene of said corresponding RNA sequence, and that contains

a maximum of 21 base pairs, which is labeled by dioxygenin.

Claim 42 (Canceled)

Claim 43 (Canceled)

Claim 44 (Currently Amended)

A nucleotide primer pair of elaim 42 comprising the a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claims 45 and 46 (canceled)

Claim 47 (Currently Amended)

A method of detecting a mycobacteria stain of

M. tuberculosis complex in a biological sample comprising

(1) contacting the biological sample to a pair of primers

5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and

5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) wherein one primer

comprises the nucleotide sequence of sequences adjacent to
the senX3-regX3 region in the 3' of senX3-region and the

other primer comprises the nucleotide sequence of sequences
adjacent to the senX3-regX3 region in the 5' of regX3

region under conditions to effect hybridization of the

primers to a nucleotide sequence the specific nucleic

acide of mycobacteria strains of M. tuberculosis complex;

(2) effecting amplification of the said nucleotide sequence

- amplified sequences from step (2) with a nucleotide probe that hybridizes at 68°C in a 5xSSC hybridization buffer with one of the sequences comprises a sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the a complement of SEQ ID No: 1, and the a complement of SEQ ID No: 2, their a corresponding RNA sequence [9] of SEQ ID No: 1, SEQ ID No: 1 or a complement of SEQ ID No: 2, a complement of SEQ ID No: 1 or a complement of SEQ ID No: 2, and that contains a maximum of 21 base pairs—under conditions for formation of hybridization complexes between—the said probe and said amplified nucleotide sequences from step (2)—of nucleic acids; and
- (4) detecting if any hybridization complexes are present, which complexes indicate the <u>a</u> presence of a mycobacteria strain of *M. tuberculosis* complex.

Claim 48 (Canceled)

Claim 49 (Currently Amended)

The method of claim 47 wherein the nucleotide probe comprises a region of SEQ ID No: 2 comprising the CAC coden in positions 40 to 42 or the complement of said region a sequence composed of nucleotides in positions 31 to 51 of SEQ ID No: 2 or a complement of said sequence.

Claim 50 (previously presented)

The method of claim 49 effected upon immunodeficient humans to differentiate an infection by BCG from an infection by a virulent mycobacterium of M. tuberculosis complex.

Claim 51 (previously presented)

The method of claim 50 wherein the human is infected with HTV.

Claim 52 (Currently Amended)

A method of identifying groups of mycobacteria belonging to a M. tuberculosis complex comprising (1) contacting the a DNA of previously extracted strains of the M. tuberculosis complex with a nucleotide primer pair comprising a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ

ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5)—of elaims 35 and 42 under conditions permitting a epecific hybridization of the primers respectively 56 base pairs upstream and 62 base pairs downstream of with one of the sequences of claim 28 a sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, a complement of SEQ ID No: 1 and a complement of SEQ ID No: 2, to obtain amplification products and (2) measuring the a length of the amplification products obtained from step (1).

Claim 53 (Canceled)

Claim 54 (Currently Amended)

A kit for in vitro identification of strains of mycobacteria of a_the_M. tuberculosis complex in a biological sample comprising (1) a primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, one primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3'of senX3 region and the other primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region a pair of primers 5'GCGCGGAGGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGGAGAACGTCAGC3' (SEQ ID No: 5).

Claim 55 (Currently Amended)

A method of detection and of differential diagnosis of BCG and the members of M. tuberculosis complex in a biological sample comprising:

- (1) contacting the biological sample to a nucleotide primer pair comprising a pair of primers

 5'GCGCAGAGACCCGAACTGC3' (SEQ ID No: 4) and

 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) for amplification of a specific nucleotide sequence of mycobacteria of M.

 tuberculosis complex, one primer comprising the nucleotide sequence of sequences adjacent to the senx3-regx3 region in the 3' of senx3 region and the other primer comprising the nucleotide sequence of sequences adjacent to the senx3-regx3 region in the 5' of regx3 region under conditions to effect hybridization of the primers to said nucleotide sequence—the specific nucleic acids of mycobacteria strains of M. tuberculosis complex;
- (2) effecting amplification of the said <u>nucleotide</u> sequence nucleic acide;
- (3) contacting the biological sample containing

 amplified nucleotide sequences from step (2) with a

 nucleotide probe of two successive sequences SEQ ID No: 1

 followed by a sequence SEQ ID No: 2 under conditions for

formation of hybridization complexes between the said probe and said amplified nucleotide sequences from step (2) of nucleic acids:

- (4) detecting any first hybridization complexes present; and
- (5) determining if said first hybridization complexes are also capable of forming second hybridization complexes with a nucleotide probe for detection of specific sequences of nucleic acids of M. tuberculosis complex other than BCG comprising a region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 sequence composed of nucleotides in positions 31 to 51 of SEQ ID No:2, or the acomplement of said sequence region, the appresence of said second hybridization complexes being indicative of the appresence of a M. tuberculosis strain different from BCG and the appresence of said first hybridization complexes uniquely being indicative of the BCG.